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Leen Beller

Life Sciences

Patentanwaltskandidatin

Nach ihrem Studium der Biomedizinischen Wissenschaften an der KU Löwen, begann Leen 2015 ihre Promotion am REGA-Institut der KU Leuven. Fünf Jahre lang untersuchte sie, wie sich die Darmflora (Darm-Mikrobiom) von gesunden Säuglingen im ersten Lebensjahr entwickelt.

Sie spezialisierte sich auf die vielen Aspekte der Mikrobiologie und Genomik, aber auch auf Bioinformatik und Biostatistik.

Berufserfahrung

- Patentanwaltskandidatin, V.O. (2021-heute)
- PhD-Studentin, Rega Institut KU Löwen (2015-2021)

Ausbildung

- PhD in Biomedical Sciences, KU Löwen (2020)
- MSc in Biomedical Sciences, KU Löwen (2015)
- BSc in Biomedical Sciences, KU Löwen (2013)

Publikationen

- Conceição-Neto, N., Zeller, M., Lefrère, H., De Bruyn, P., Beller, L., Deboutte, W., Yinda, C. K., Lavigne, R., Maes, P., Ranst, M. Van, Heylen, E. & Matthijnsens, J. Modular approach to customise sample preparation procedures for viral metagenomics: A reproducible protocol for virome analysis. *Sci. Rep.* 5, 16532 (2015).
- Yinda, C. K., Zeller, M., Conceição-Neto, N., Maes, P., Deboutte, W., Beller, L., Heylen, E., Ghogomu, S. M., Van Ranst, M. & Matthijnsens, J. Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. *Sci. Rep.* 6, 34209 (2016).
- Yinda, C. K., Ghogomu, S. M., Conceição-Neto, N., Beller, L., Deboutte, W., Vanhulle, E., Maes, P., Van Ranst, M. & Matthijnsens, J. Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. *Virus Evol.* 4, vey008 (2018).
- Theuns, S., Vanmechelen, B., Bernaert, Q., Deboutte, W., Vandenhole, M., Beller, L., Matthijnsens, J., Maes, P. & Nauwynck, H. J. Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. *Sci. Rep.* 8, 9830 (2018).
- Vanmechelen, B., Bletsas, M., Laenen, L., Lopes, A. R., Vergote, V., Beller, L., Deboutte, W., Korva, M., Avšič Županc, T., Goüy de Bellocq, J., Gryseels, S., Leirs, H., Lemey, P., Vrancken, B. & Maes, P. Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. *BMC Genomics* 19, 617 (2018).
- Yinda, C. K., Vanhulle, E., Conceição-Neto, N., Beller, L., Deboutte, W., Shi, C., Ghogomu, S. M., Maes, P.,

Van Ranst, M. & Matthijnsens, J. Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. *mSphere* 4, (2019).

- Beller, L. & Matthijnsens, J. What is (not) known about the dynamics of the human gut virome in health and disease. *Curr. Opin. Virol.* 37, 52–57 (2019).
- Shi, C., Beller, L., Deboutte, W., Yinda, K. C., Delang, L., Vega-Rúa, A., Failloux, A.-B. & Matthijnsens, J. Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. *Microbiome* 7, 121 (2019).
- Wollants, E., Beller, L., Beuselinck, K., Bloemen, M., Lagrou, K., Reynders, M. & Van Ranst, M. A decade of enterovirus genetic diversity in Belgium. *J. Clin. Virol.* 121, 104205 (2019).
- Deboutte, W., Beller, L., Yinda, C. K., Maes, P., de Graaf, D. C. & Matthijnsens, J. Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. *Proc. Natl. Acad. Sci. U. S. A.* 117, 10511–10519 (2020).
- Thijssen, M., Tacke, F., Beller, L., Deboutte, W., Yinda, K. C., Nevens, F., Laleman, W., Van Ranst, M. & Pourkarim, M. R. Clinical relevance of plasma virome dynamics in liver transplant recipients. *EBioMedicine* 60, 103009 (2020).
- Simsek, C., Corman, V. M., Everling, H. U., Lukashev, A. N., Rasche, A., Maganga, G. D., Binger, T., Jansen, D., Beller, L., Deboutte, W., Gloza-Rausch, F., Seebens-Hoyer, A., Yordanov, S., Sylverken, A., Oppong, S., Sarkodie, Y. A., Vallo, P., Leroy, E. M., Bourgarel, M., Yinda, K. C., Van Ranst, M., Drosten, C., Drexler, J. F. & Matthijnsens, J. At least seven distinct rotavirus genotype constellations in bats with evidence of reassortment and zoonotic transmissions. *MBio* 12, (2021).

Sprachen

- Niederländisch (Muttersprache)
- Englisch (tüchtig)
- Französisch (basic)